SEQUENCE LISTING

<110> The Scripps Research Institute
      The Regents of the University of California
      Wu, Eugene
      Nemerow, Glen R.
      Stewart, Phoebe

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<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 25
tgtacaccgg atccggcgca cacc                                        24

<210> 26
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 26
cacaacgagc tcaattaatt aattgccaca tcctc                            35

<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 27
cgcgctgact cttaaggact agtttc                                      26

<210> 28
<211> 37
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<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 28
gcgcttaatt aacatcatca ataatatacc ttatttt                                    37

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 29
atcatggccg acaagcagaa gaac                                                  24

<210> 30
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 30
gtacagctcg tccatgccga gagt                                                  24

<210> 31
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> EGFP probe

<221> misc_feature
<222> 1
<223> FAM (6-carboxy-fluorescein)

<221> misc_feature
<222> 26
<223> TAMRA (6-carboxy-tetramethyl-rhodamine)

<400> 31
caggaccatg tgatcgcgct tctcgt                                                26

<210> 32
<211> 1749
<212> DNA
<213> Adenovirus serotype 2 fiber

<220>
<221> CDS
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<222> (1)...(1749)

<400> 32
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atg aaa cgc gcc aga ccg tct gaa gac acc ttc aac ccc gtg tat cca    48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                   10                  15

tat gac aca gaa acc ggg cct cca act gtg ccc ttt ctt acc cct cca    96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
                20                  25                  30

ttt gtt tca ccc aat ggt ttc caa gaa agt ccc cct gga gtt ctc tct   144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
            35                  40                  45

cta cgc gtc tcc gaa cct ttg gac acc tcc cac ggc atg ctt gcg ctt   192
Leu Arg Val Ser Glu Pro Leu Asp Thr Ser His Gly Met Leu Ala Leu
        50                  55                  60

aaa atg ggc agc ggt ctt acc cta gac aag gcc gga aac ctc acc tcc   240
Lys Met Gly Ser Gly Leu Thr Leu Asp Lys Ala Gly Asn Leu Thr Ser
 65                  70                  75                  80

caa aat gta acc act gtt act cag cca ctt aaa aaa aca aag tca aac   288
Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys Lys Thr Lys Ser Asn
                85                  90                  95

ata agt ttg gac acc tcc gca cca ctt aca att acc tca ggc gcc cta   336
Ile Ser Leu Asp Thr Ser Ala Pro Leu Thr Ile Thr Ser Gly Ala Leu
                100                 105                 110

aca gtg gca acc acc gct cct ctg ata gtt act agc ggc gct ctt agc   384
Thr Val Ala Thr Thr Ala Pro Leu Ile Val Thr Ser Gly Ala Leu Ser
        115                 120                 125

gta cag tca caa gcc cca ctg acc gtg caa gac tcc aaa cta agc att   432
Val Gln Ser Gln Ala Pro Leu Thr Val Gln Asp Ser Lys Leu Ser Ile
    130                 135                 140

gct act aaa ggg ccc att aca gtg tca gat gga aag cta gcc ctg caa   480
Ala Thr Lys Gly Pro Ile Thr Val Ser Asp Gly Lys Leu Ala Leu Gln
145                 150                 155                 160

aca tca gcc ccc ctc tct ggc agt gac agc gac acc ctt act gta act   528
Thr Ser Ala Pro Leu Ser Gly Ser Asp Ser Asp Thr Leu Thr Val Thr
                165                 170                 175

gca tca ccc ccg cta act act gcc acg ggt agc ttg ggc att aac atg   576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asn Met
            180                 185                 190

gaa gat cct att tat gta aat aat gga aaa ata gga att aaa ata agc   624
Glu Asp Pro Ile Tyr Val Asn Asn Gly Lys Ile Gly Ile Lys Ile Ser
            195                 200                 205

ggt cct ttg caa gta gca caa aac tcc gat aca cta aca gta gtt act   672
Gly Pro Leu Gln Val Ala Gln Asn Ser Asp Thr Leu Thr Val Val Thr
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gga cca ggt gtc acc gtt gaa caa aac tcc ctt aga acc aaa gtt gca   720
Gly Pro Gly Val Thr Val Glu Gln Asn Ser Leu Arg Thr Lys Val Ala
225   230   235   240

gga gct att ggt tat gat tca tca aac aac atg gaa att aaa acg ggc   768
Gly Ala Ile Gly Tyr Asp Ser Ser Asn Asn Met Glu Ile Lys Thr Gly
                245   250   255

ggt ggc atg cgt ata aat aac aac ttg tta att cta gat gtg gat tac   816
Gly Gly Met Arg Ile Asn Asn Asn Leu Leu Ile Leu Asp Val Asp Tyr
                260   265   270

cca ttt gat gct caa aca aaa cta cgt ctt aaa ctg ggg cag gga ccc   864
Pro Phe Asp Ala Gln Thr Lys Leu Arg Leu Lys Leu Gly Gln Gly Pro
                275   280   285

ctg tat att aat gca tct cat aac ttg gac ata aac tat aac aga ggc   912
Leu Tyr Ile Asn Ala Ser His Asn Leu Asp Ile Asn Tyr Asn Arg Gly
                290   295   300

cta tac ctt ttt aat gca tca aac aat act aaa aaa ctg gaa gtt agc   960
Leu Tyr Leu Phe Asn Ala Ser Asn Asn Thr Lys Lys Leu Glu Val Ser
305   310   315   320

ata aaa aaa tcc agt gga cta aac ttt gat aat act gcc ata gct ata   1008
Ile Lys Lys Ser Ser Gly Leu Asn Phe Asp Asn Thr Ala Ile Ala Ile
                325   330   335

aat gca gga aag ggt ctg gag ttt gat aca aac aca tct gag tct cca   1056
Asn Ala Gly Lys Gly Leu Glu Phe Asp Thr Asn Thr Ser Glu Ser Pro
                340   345   350

gat atc aac cca ata aaa act aaa att ggc tct ggc att gat tac aat   1104
Asp Ile Asn Pro Ile Lys Thr Lys Ile Gly Ser Gly Ile Asp Tyr Asn
                355   360   365

gaa aac ggt gcc atg att act aaa ctt gga gcg ggt tta agc ttt gac   1152
Glu Asn Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp
370   375   380

aac tca ggg gcc att aca ata gga aac aaa aat gat gac aaa ctt acc   1200
Asn Ser Gly Ala Ile Thr Ile Gly Asn Lys Asn Asp Asp Lys Leu Thr
385   390   395   400

ctg tgg aca acc cca gac cca tct cct aac tgc aga att cat tca gat   1248
Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile His Ser Asp
                405   410   415

aat gac tgc aaa ttt act ttg gtt ctt aca aaa tgt ggg agt caa gta   1296
Asn Asp Cys Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val
                420   425   430

cta gct act gta gct gct ttg gct gta tct gga gat ctt tca tcc atg   1344
Leu Ala Thr Val Ala Ala Leu Ala Val Ser Gly Asp Leu Ser Ser Met
                435   440   445

```
aca ggc acc gtt gca agt gtt agt ata ttc ctt aga ttt gac caa aac    1392
Thr Gly Thr Val Ala Ser Val Ser Ile Phe Leu Arg Phe Asp Gln Asn
    450                 455                 460

ggt gtt cta atg gag aac tcc tca ctt aaa aaa cat tac tgg aac ttt    1440
Gly Val Leu Met Glu Asn Ser Ser Leu Lys Lys His Tyr Trp Asn Phe
465                 470                 475                 480

aga aat ggg aac tca act aat gca aat cca tac aca aat gca gtt gga    1488
Arg Asn Gly Asn Ser Thr Asn Ala Asn Pro Tyr Thr Asn Ala Val Gly
                    485                 490                 495

ttt atg cct aac ctt cta gcc tat cca aaa acc caa agt caa act gct    1536
Phe Met Pro Asn Leu Leu Ala Tyr Pro Lys Thr Gln Ser Gln Thr Ala
                500                 505                 510

aaa aat aac att gtc agt caa gtt tac ttg cat ggt gat aaa act aaa    1584
Lys Asn Asn Ile Val Ser Gln Val Tyr Leu His Gly Asp Lys Thr Lys
            515                 520                 525

cct atg ata ctt acc att aca ctt aat ggc act agt gaa tcc aca gaa    1632
Pro Met Ile Leu Thr Ile Thr Leu Asn Gly Thr Ser Glu Ser Thr Glu
    530                 535                 540

act agc gag gta agc act tac tct atg tct ttt aca tgg tcc tgg gaa    1680
Thr Ser Glu Val Ser Thr Tyr Ser Met Ser Phe Thr Trp Ser Trp Glu
545                 550                 555                 560

agt gga aaa tac acc act gaa act ttt gct acc aac tct tac acc ttc    1728
Ser Gly Lys Tyr Thr Thr Glu Thr Phe Ala Thr Asn Ser Tyr Thr Phe
                565                 570                 575

tcc tac att gcc cag gaa taa                                         1749
Ser Tyr Ile Ala Gln Glu  *
                580


<210> 33
<211> 582
<212> PRT
<213> Adenovirus serotype 2 fiber

<400> 33
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45
Leu Arg Val Ser Glu Pro Leu Asp Thr Ser His Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Ser Gly Leu Thr Leu Asp Lys Ala Gly Asn Leu Thr Ser
65                  70                  75                  80
Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys Lys Thr Lys Ser Asn
                85                  90                  95
Ile Ser Leu Asp Thr Ser Ala Pro Leu Thr Ile Thr Ser Gly Ala Leu
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                100                     105                     110
Thr Val Ala Thr Thr Ala Pro Leu Ile Val Thr Ser Gly Ala Leu Ser
        115                     120                     125
Val Gln Ser Gln Ala Pro Leu Thr Val Gln Asp Ser Lys Leu Ser Ile
    130                     135                     140
Ala Thr Lys Gly Pro Ile Thr Val Ser Asp Gly Lys Leu Ala Leu Gln
145                     150                     155                     160
Thr Ser Ala Pro Leu Ser Gly Ser Asp Ser Asp Thr Leu Thr Val Thr
                165                     170                     175
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asn Met
                180                     185                     190
Glu Asp Pro Ile Tyr Val Asn Asn Gly Lys Ile Gly Ile Lys Ile Ser
            195                     200                     205
Gly Pro Leu Gln Val Ala Gln Asn Ser Asp Thr Leu Thr Val Val Thr
        210                     215                     220
Gly Pro Gly Val Thr Val Glu Gln Asn Ser Leu Arg Thr Lys Val Ala
225                     230                     235                     240
Gly Ala Ile Gly Tyr Asp Ser Ser Asn Asn Met Glu Ile Lys Thr Gly
                245                     250                     255
Gly Gly Met Arg Ile Asn Asn Asn Leu Leu Ile Leu Asp Val Asp Tyr
            260                     265                     270
Pro Phe Asp Ala Gln Thr Lys Leu Arg Leu Lys Leu Gly Gln Gly Pro
            275                     280                     285
Leu Tyr Ile Asn Ala Ser His Asn Leu Asp Ile Asn Tyr Asn Arg Gly
    290                     295                     300
Leu Tyr Leu Phe Asn Ala Ser Asn Asn Thr Lys Lys Leu Glu Val Ser
305                     310                     315                     320
Ile Lys Lys Ser Ser Gly Leu Asn Phe Asp Asn Thr Ala Ile Ala Ile
                325                     330                     335
Asn Ala Gly Lys Gly Leu Glu Phe Asp Thr Asn Thr Ser Glu Ser Pro
            340                     345                     350
Asp Ile Asn Pro Ile Lys Thr Lys Ile Gly Ser Gly Ile Asp Tyr Asn
    355                     360                     365
Glu Asn Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp
    370                     375                     380
Asn Ser Gly Ala Ile Thr Ile Gly Asn Lys Asn Asp Asp Lys Leu Thr
385                     390                     395                     400
Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile His Ser Asp
                405                     410                     415
Asn Asp Cys Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val
            420                     425                     430
Leu Ala Thr Val Ala Ala Leu Ala Val Ser Gly Asp Leu Ser Ser Met
        435                     440                     445
Thr Gly Thr Val Ala Ser Val Ser Ile Phe Leu Arg Phe Asp Gln Asn
    450                     455                     460
Gly Val Leu Met Glu Asn Ser Ser Leu Lys Lys His Tyr Trp Asn Phe
465                     470                     475                     480
Arg Asn Gly Asn Ser Thr Asn Ala Asn Pro Tyr Thr Asn Ala Val Gly
            485                     490                     495
Phe Met Pro Asn Leu Leu Ala Tyr Pro Lys Thr Gln Ser Gln Thr Ala
            500                     505                     510
Lys Asn Asn Ile Val Ser Gln Val Tyr Leu His Gly Asp Lys Thr Lys
    515                     520                     525
Pro Met Ile Leu Thr Ile Thr Leu Asn Gly Thr Ser Glu Ser Thr Glu
    530                     535                     540
Thr Ser Glu Val Ser Thr Tyr Ser Met Ser Phe Thr Trp Ser Trp Glu
545                     550                     555                     560
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Ser Gly Lys Tyr Thr Thr Glu Thr Phe Ala Thr Asn Ser Tyr Thr Phe
                565                  570                  575
Ser Tyr Ile Ala Gln Glu
            580


<210> 34
<211> 1746
<212> DNA
<213> Adenovirus serotype 5 fiber

<220>
<221> CDS
<222> (1)...(1746)

<400> 34
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca      48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                  10                  15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc      96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
             20                  25                  30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct     144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
         35                  40                  45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc     192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
     50                  55                  60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc     240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65                  70                  75                  80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac     288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                 85                  90                  95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta     336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
             100                 105                 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc     384
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
         115                 120                 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att     432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
     130                 135                 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa     480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act     528
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Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
            165                     170                 175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg      576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180                     185                 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg      624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
            195                     200                 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act      672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
    210                     215                 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act      720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225                     230                 235                 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca      768
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                245                     250                 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt      816
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
            260                     265                 270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag      864
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
            275                     280                 285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac      912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290                     295                 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag      960
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305         .           310                 315                 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata     1008
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
            325                     330                 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca     1056
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
            340                     345                 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat     1104
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
            355                     360                 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac     1152
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370                     375                 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act     1200
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
```

			385			390				395				400		

```
                    385                     390                      395                       400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag      1248
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                405             410                 415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata      1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
                420             425                 430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata      1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
                435             440                 445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat      1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
    450             455                 460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt      1440
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465             470                 475                 480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga      1488
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
                485                 490                 495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc      1536
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
                500                 505                 510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa      1584
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
                515                 520                 525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac      1632
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
    530                 535                 540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc      1680
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545                 550                 555                 560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca      1728
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
                565                 570                 575

tac att gcc caa gaa taa                                              1746
Tyr Ile Ala Gln Glu  *
                580
```

<210> 35
<211> 581
<212> PRT
<213> Adenovirus serotype 5 fiber

<400> 35

```
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                   10                  15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70                  75                  80
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
            85                  90                  95
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
        100                 105                 110
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
        115                 120                 125
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130                 135                 140
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                 160
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
            165                 170                 175
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
        180                 185                 190
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
        195                 200                 205
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
    210                 215                 220
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225                 230                 235                 240
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
            245                 250                 255
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
        260                 265                 270
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
    275                 280                 285
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290                 295                 300
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305                 310                 315                 320
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
            325                 330                 335
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
        340                 345                 350
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355                 360                 365
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370                 375                 380
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385                 390                 395                 400
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
            405                 410                 415
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
        420                 425                 430
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
        435                 440                 445
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
```

```
        450                   455                   460
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465                   470                   475                   480
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
                485                   490                   495
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
            500                   505                   510
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
            515                   520                   525
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
        530                   535                   540
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545                   550                   555                   560
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
                565                   570                   575
Tyr Ile Ala Gln Glu
                580
```

<210> 36
<211> 1098
<212> DNA
<213> Adenovirus serotype 37 fiber

<220>
<221> CDS
<222> (1)...(1098)

<400> 36
```
atg tca aag agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc    48
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
1               5                   10                  15

tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt    96
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
                20                  25                  30

gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg gta ctg tca ctc   144
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
            35                  40                  45

aaa ctg gct gat cca atc acc att acc aat ggg gat gta tcc ctc aag   192
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
    50                  55                  60

gtg gga ggt ggt ctc act ttg caa gat gga agc cta act gta aac cct   240
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
65                  70                  75                  80

aag gct cca ctg caa gtt aat act gat aaa aaa ctt gag ctt gca tat   288
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr
                85                  90                  95

gat aat cca ttt gaa agt agt gct aat aaa ctt agt tta aaa gta gga   336
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
                100                 105                 110
```

```
cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat     384
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
        115                     120                 125

tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa     432
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
        130                     135                 140

aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta     480
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145                     150                 155                 160

aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca     528
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
                    165                 170                 175

tgg aac cca aag tat gac acg cgc aca ctt tgg aca aca cca gac aca     576
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
                180                 185                 190

tct cca aac tgc aca att gct caa gat aag gac tct aaa ctc act ttg     624
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu
                195                 200                 205

gta ctt aca aag tgt gga agt caa ata tta gct aat gtg tct ttg att     672
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
        210                 215                 220

gtg gtc gca gga aag tac cac atc ata aat aat aag aca aat cca aaa     720
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Lys
225                 230                 235                 240

ata aaa agt ttt act att aaa ctg cta ttt aat aag aac gga gtg ctt     768
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
                245                 250                 255

tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga     816
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
                260                 265                 270

aat tcc aat gtt tcg aca gct tat gaa aaa gca att ggt ttt atg cct     864
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
                275                 280                 285

aat ttg gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga     912
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
        290                 295                 300

gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca     960
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
305                 310                 315                 320

gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct    1008
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
                325                 330                 335

atc aca ttt aac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt    1056
```

```
Ile Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
            340                 345                 350

gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga              1098
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu  *
            355                 360                 365
```

<210> 37
<211> 365
<212> PRT
<213> Adenovirus serotype 37 fiber

<400> 37

```
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
            20                  25                  30
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
            35                  40                  45
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
    50                  55                  60
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
65                  70                  75                  80
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr
                85                  90                  95
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
            100                 105                 110
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
            115                 120                 125
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
    130                 135                 140
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145                 150                 155                 160
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
                165                 170                 175
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
            180                 185                 190
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu
            195                 200                 205
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
    210                 215                 220
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Lys
225                 230                 235                 240
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
                245                 250                 255
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
            260                 265                 270
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
            275                 280                 285
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
    290                 295                 300
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
305                 310                 315                 320
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
                325                 330                 335
```

Ile Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
        340   345   350
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
        355   360   365

<210> 38
<211> 1098
<212> DNA
<213> Adenovirus serotype 19p fiber

<220>
<221> CDS
<222> (1)...(1098)

<400> 38
atg tca aag agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc   48
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
1   5   10   15

tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt   96
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
                20   25   30

gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg gta ctg tca ctc   144
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
            35   40   45

aaa ctg gct gat cca atc acc att acc aat ggg gat gta tcc ctc aag   192
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
        50   55   60

gtg gga ggt ggt ctc act ttg caa gat gga agc cta act gta aac cct   240
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
65   70   75   80

aag gct cca ctg caa gtt act act gat aaa aaa ctt gag ctt gca tat   288
Lys Ala Pro Leu Gln Val Thr Thr Asp Lys Lys Leu Glu Leu Ala Tyr
                85   90   95

gat aat cca ttt gaa tgt agt gct aat aaa ttt agt tta aaa gta gga   336
Asp Asn Pro Phe Glu Cys Ser Ala Asn Lys Phe Ser Leu Lys Val Gly
                100   105   110

cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat   384
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
            115   120   125

tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa   432
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
        130   135   140

aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta   480
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145   150   155   160

aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca   528

```
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
            165                 170                 175

tgg aac cca aag tat gac acg cgc aca ctt tgg aca aca cca gac aca    576
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
            180                 185                 190

tct cca aac tgc aca att gct cag gat aag gac tct aaa ctc act ttg    624
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu
            195                 200                 205

gta ctt aca aag tgt gga agt caa ata tta gct aat gtg tct ttg att    672
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
    210                 215                 220

gtg gtc gca gga aag tac cac atc ata aat aat aag aca aat cca gaa    720
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Glu
225                 230                 235                 240

ata aaa agt ttt act att aaa ctg tta ttt aat aag aac gga gtg ctt    768
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
                245                 250                 255

tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga    816
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
            260                 265                 270

aat tcc aat gtt tcg aca gct tat gaa aaa gca att ggt ttt atg cct    864
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
            275                 280                 285

aat tta gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga    912
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
        290                 295                 300

gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca    960
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
305                 310                 315                 320

gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct   1008
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
                325                 330                 335

atc aca ttt gac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt   1056
Ile Thr Phe Asp Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
                340                 345                 350

gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga           1098
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu *
            355                 360                 365
```

<210> 39
<211> 365
<212> PRT
<213> Adenovirus serotype 19p fiber

<400> 39

```
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
1               5                   10                  15
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
            20                  25                  30
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
        35                  40                  45
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
        50                  55                  60
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
65                  70                  75                  80
Lys Ala Pro Leu Gln Val Thr Thr Asp Lys Lys Leu Glu Leu Ala Tyr
                85                  90                  95
Asp Asn Pro Phe Glu Cys Ser Ala Asn Lys Phe Ser Leu Lys Val Gly
            100                 105                 110
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
        115                 120                 125
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
        130                 135                 140
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145                 150                 155                 160
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
                165                 170                 175
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
            180                 185                 190
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu
            195                 200                 205
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
    210                 215                 220
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Glu
225                 230                 235                 240
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
            245                 250                 255
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
            260                 265                 270
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
        275                 280                 285
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
    290                 295                 300
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
305                 310                 315                 320
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
            325                 330                 335
Ile Thr Phe Asp Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
            340                 345                 350
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
            355                 360                 365
```

<210> 40
<211> 1228
<212> DNA
<213> Adenovirus serotype 9 fiber

<220>
<221> CDS

```
aagggatgtc aaattcctgg tccacaattt tcattgtctt ccctctcag atg tca aag  58
                                                        Met Ser Lys
                                                          1 .
```

```
agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc tat ggc tac  106
Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro Tyr Gly Tyr
      5               10                  15
```

```
gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt gtc tcc tcc  154
Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser
 20                  25                  30                  35
```

```
gat gga ttc caa aac ttc ccc cct ggg gtc ctg tca ctc aaa cta gct  202
Asp Gly ·Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala
              40                  45                  50
```

```
gac cca ata gcc atc gtc aat ggg aat gtc tca ctc aaa gtg gga ggg  250
Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys Val Gly Gly
              55                  60                  65
```

```
ggt ctc act ttg caa gat gga act gga aaa cta aca gtc aat gct gat  298
Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val Asn Ala Asp
          70                  75                  80
```

```
cca cct ttg caa ctt aca aac aac aaa tta ggg att gct ttg gac gct  346
Pro Pro Leu Gln Leu Thr Asn Asn Lys Leu Gly Ile Ala Leu Asp Ala
      85                  90                  95
```

```
cca ttt gat gtt ata gat aat aaa ctc aca ttg tta gcg ggc cat ggc  394
Pro Phe Asp Val Ile Asp Asn Lys Leu Thr Leu Leu Ala Gly His Gly
100                 105                 110                 115
```

```
ttg tct att ata aca aaa gaa aca tca aca ctg cct ggc ttg agg aat  442
Leu Ser Ile Ile Thr Lys Glu Thr Ser Thr Leu Pro Gly Leu Arg Asn
              120                 125                 130
```

```
act ctt gta gta tta act gga aag ggt att gga aca gaa tca aca gat  490
Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu Ser Thr Asp
          135                 140                 145
```

```
aat ggc gga acg gta tgt gtt aga gtt gga gaa ggt ggc ggc tta tca  538
Asn Gly Gly Thr Val Cys Val Arg Val Gly Glu Gly Gly Gly Leu Ser
          150                 155                 160
```

```
ttt aat aat gat gga gac ttg gta gca ttt aat aaa aaa gaa gat aag  586
Phe Asn Asn Asp Gly Asp Leu Val Ala Phe Asn Lys Lys Glu Asp Lys
          165                 170                 175
```

```
cgc acc cta tgg aca act cca gac aca tct cca aat tgc aag att gat  634
Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Lys Ile Asp
180                 185             .       190                 195
```

```
cag gat aag gac tct aag tta act ctg gtc ctt aca aag tgt gga agt  682
Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser
```

```
caa ata ttg gct aat gtg tca tta att gtc gta gat ggt aag tac aaa   730
Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Asp Gly Lys Tyr Lys
        215                 220                 225

att atc aat aac aat act caa cca gct ctc aaa gga ttt acc att aaa   778
Ile Ile Asn Asn Asn Thr Gln Pro Ala Leu Lys Gly Phe Thr Ile Lys
        230                 235                 240

tta ttg ttt gat gaa aat gga gta ctt atg gaa tct tca aat ctt ggt   826
Leu Leu Phe Asp Glu Asn Gly Val Leu Met Glu Ser Ser Asn Leu Gly
        245                 250                 255

aaa tca tat tgg aac ttt aga aat gaa aat tca att atg tca aca gct   874
Lys Ser Tyr Trp Asn Phe Arg Asn Glu Asn Ser Ile Met Ser Thr Ala
260                 265                 270                 275

tat gaa aaa gct att gga ttc atg cct aat ttg gta gcc tat cca aaa   922
Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro Lys
                280                 285                 290

cct acc gct ggc tct aaa aaa tat gca aga gat ata gtt tat gga aac   970
Pro Thr Ala Gly Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Asn
                295                 300                 305

atc tac ctt ggt gga aag cca gat caa cca gta acc att aaa act acc  1018
Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Val Thr Ile Lys Thr Thr
        310                 315                 320

ttt aat cag gaa act gga tgt gaa tat tct atc aca ttt gat ttt agt  1066
Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asp Phe Ser
    325                 330                 335

tgg gcc aag act tat gta aat gtt gaa ttt gaa aca acc tct ttt acc  1114
Trp Ala Lys Thr Tyr Val Asn Val Glu Phe Glu Thr Thr Ser Phe Thr
340                 345                 350                 355

ttt tcc tat atc gcc caa gaa tga aagaccaata aacgtgtttt tcatttcaaa  1168
Phe Ser Tyr Ile Ala Gln Glu  *
                360

attttcatgt atctttattg atttttacac cagcacgggt agtcagtctc ccaccaccag 1228
```

```
<210> 41
<211> 362
<212> PRT
<213> Adenovirus serotype 9 fiber

<400> 41
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1               5                   10                  15
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
            20                  25                  30
Val Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu
        35                  40                  45
```

```
Lys Leu Ala Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys
    50                  55                  60
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val
65                  70                  75                  80
Asn Ala Asp Pro Pro Leu Gln Leu Thr Asn Asn Lys Leu Gly Ile Ala
                85                  90                  95
Leu Asp Ala Pro Phe Asp Val Ile Asp Asn Lys Leu Thr Leu Leu Ala
                100                 105                 110
Gly His Gly Leu Ser Ile Ile Thr Lys Glu Thr Ser Thr Leu Pro Gly
        115                 120                 125
Leu Arg Asn Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
    130                 135                 140
Ser Thr Asp Asn Gly Gly Thr Val Cys Val Arg Val Gly Glu Gly Gly
145                 150                 155                 160
Gly Leu Ser Phe Asn Asn Asp Gly Asp Leu Val Ala Phe Asn Lys Lys
                165                 170                 175
Glu Asp Lys Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys
                180                 185                 190
Lys Ile Asp Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys
                195                 200                 205
Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Asp Gly
    210                 215                 220
Lys Tyr Lys Ile Ile Asn Asn Asn Thr Gln Pro Ala Leu Lys Gly Phe
225                 230                 235                 240
Thr Ile Lys Leu Leu Phe Asp Glu Asn Gly Val Leu Met Glu Ser Ser
                245                 250                 255
Asn Leu Gly Lys Ser Tyr Trp Asn Phe Arg Asn Glu Asn Ser Ile Met
        260                 265                 270
Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala
        275                 280                 285
Tyr Pro Lys Pro Thr Ala Gly Ser Lys Lys Tyr Ala Arg Asp Ile Val
    290                 295                 300
Tyr Gly Asn Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Val Thr Ile
305                 310                 315                 320
Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe
                325                 330                 335
Asp Phe Ser Trp Ala Lys Thr Tyr Val Asn Val Glu Phe Glu Thr Thr
                340                 345                 350
Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
        355                 360
```

```
<210> 42
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad2   third repeat

<400> 42
Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys
  1                 5                   10                  15
Lys Thr Lys Ser
            20
```

```
<210> 43
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5  third repeat

<400> 43
Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys
 1               5                   10                  15
Lys Thr Lys Ser
            20


<210> 44
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Repeat motif

<221> VARIANT
<222> 4
<223> Xaa = Thr or Ser

<400> 44
Thr Thr Val Xaa
 1


<210> 45
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Repeat Consensus Sequence

<221> VARIANT
<222> 3,5,7,13
<223> Xaa = Hydrophobic Amino Acid

<221> VARIANT
<222> 1, 2, 4,  6, 8, 9, 11, 12, 14, 15
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 10
<223> Xaa = Pro or Gly

<400> 45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5                   10                  15
```

<210> 46
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad2 21st repeat

<400> 46
Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp Asn Ser
 1   5   10   15

<210> 47
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5 21st repeat

<400> 47
Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp Ser Thr
 1   5   10   15

<210> 48
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad37 last repeat

<400> 48
Ile Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp
 1   5   10   15

<210> 49
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Last repeat consensus sequence

<221> VARIANT
<222> 4,7
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 9
<223> Xaa = Asp or Asn

<400> 49
Lys Leu Gly Xaa Gly Leu Xaa Phe Xaa

<210> 50
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad5Ds fiber

<221> CDS
<222> (13)...(1092)

<221> misc_feature
<222> 1130, 1157
<223> n = A,T,C or G

<400> 50

```
atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc  51
              Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
               1             5                  10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt     99
Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
     15                  20                  25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg    147
Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
 30                  35                  40                  45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg    195
Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
             50                  55                  60

ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac  · 243
Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn
                 65                  70                  75

ctt acc tcc caa aat gta acc act gtg agc cca cct ctc aaa aaa acc    291
Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr
             80                  85                  90

aag aaa aag ctt gaa gtt aac cta agc act gcc aag ggg ttg atg ttt    339
Lys Lys Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe
         95                  100                 105

gac gct aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt    387 ·
Asp Ala Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly
110                 115                 120                 125

tca cct aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat    435
Ser Pro Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His
                 130                 135                 140

ggc cta gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act    483
Gly Leu Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr
```

```
                145                    150                    155

ggc ctt agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat   531
Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn
        160                    165                    170

aat gat aag cta act ttg tgg acc aca cca gct cca tct cct aac tgt   579
Asn Asp Lys Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys
        175                    180                    185

aga cta aat gca gag aaa gat gct aaa ctc act ttg gtc tta aca aaa   627
Arg Leu Asn Ala Glu Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys
190                    195                    200                    205

tgt ggc agt caa ata ctt gct aca gtt tca gtt ttg gct gtt aaa ggc   675
Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly
                    210                    215                    220

agt ttg gct cca ata tct gga aca gtt caa agt gct cat ctt att ata   723
Ser Leu Ala Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile
                225                    230                    235

aga ttt gac gaa aat gga gtg cta cta aac aat tcc ttc ctg gac cca   771
Arg Phe Asp Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro
        240                    245                    250

gaa tat tgg aac ttt aga aat gga gat ctt act gaa ggc aca gcc tat   819
Glu Tyr Trp Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr
        255                    260                    265

aca aac gct gtt gga ttt atg cct aac cta tca gct tat cca aaa tct   867
Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser
270                    275                    280                    285

cac ggt aaa act gcc aaa agt aac att gtc agt caa gtt tac tta aac   915
His Gly Lys Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn
                    290                    295                    300

gga gac aaa act aaa cct gta aca cta acc att aca cta aac ggt aca   963
Gly Asp Lys Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr
                305                    310                    315

cag gaa aca gga gac aca act cca agt gca tac tct atg tca ttt tca   1011
Gln Glu Thr Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser
        320                    325                    330

tgg gac tgg tct ggc cac aac tac att aat gaa ata ttt gcc aca tcc   1059
Trp Asp Trp Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser
        335                    340                    345

tct tac act ttt tca tac att gcc caa gaa taa agaagcggcc gcgttatgaa   1112
Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu  *
350                    355

gggcgaattc cagcacantg gcggccgtta ttagtggatc cgagntcatg ca          1164

<210> 51
```

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5deltas

<400> 51
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Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70                  75                  80
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Lys Lys
                85                  90                  95
Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr
            100                 105                 110
Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn
        115                 120                 125
Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu
    130                 135                 140
Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser
145                 150                 155                 160
Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys
                165                 170                 175
Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn
            180                 185                 190
Ala Glu Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser
        195                 200                 205
Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala
    210                 215                 220
Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp
225                 230                 235                 240
Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp
                245                 250                 255
Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala
            260                 265                 270
Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys
        275                 280                 285
Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys
    290                 295                 300
Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr
305                 310                 315                 320
Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp
                325                 330                 335
Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr
            340                 345                 350
Phe Ser Tyr Ile Ala Gln Glu
            355
```

<210> 52

<211> 1920
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad5s/Ad37k fiber

<221> CDS
<222> (13)...(1755)

<221> misc_feature
<222> 1867, 1875
<223> n = A,T,C or G

<400> 52
gcaagatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
            Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
            1   5   10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
    15   20   25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
 30   35   40   45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg 195
Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
          50   55   60

ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac 243
Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn
          65   70   75

ctt acc tcc caa aat gta acc act gtg agc cca cct ctc aaa aaa acc 291
Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr
      80   85   90

aag tca aac ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca 339
Lys Ser Asn Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser
    95   100   105

gaa gcc cta act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac 387
Glu Ala Leu Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn
110   115   120   125

aca ctc acc atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa 435
Thr Leu Thr Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys
          130   135   140

ctt agc att gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta 483
Leu Ser Ile Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu
          145   150   155

gcc ctg caa aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt 531
Ala Leu Gln Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu

```
              160                   165                    170

act atc act gcc tca ccc cct cta act act gcc act ggt agc ttg ggc    579
Thr Ile Thr Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly
    175             180                 185

att gac ttg aaa gag ccc att tat aca caa aat gga aaa cta gga cta    627
Ile Asp Leu Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu
190             195                 200                 205

aag tac ggg gct cct ttg cat gta aca gac gac cta aac act ttg acc    675
Lys Tyr Gly Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr
                210             215                 220

gta gca act ggt cca ggt gtg act att aat aat act tcc ttg caa act    723
Val Ala Thr Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr
            225             230                 235

aaa gtt act gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt    771
Lys Val Thr Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu
        240             245                 250

aat gta gca gga gga cta agg att gat tct caa aac aga cgc ctt ata    819
Asn Val Ala Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile
    255             260                 265

ctt gat gtt agt tat ccg ttt gat gct caa aac caa cta aat cta aga    867
Leu Asp Val Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg
270             275                 280                 285

cta gga cag ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att    915
Leu Gly Gln Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile
                290             295                 300

aac tac aac aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa    963
Asn Tyr Asn Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys
            305             310                 315

aag ctt gag gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct   1011
Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala
        320             325                 330

aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct   1059
Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro
    335             340                 345

aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta   1107
Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu
350             355                 360                 365

gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act ggc ctt   1155
Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu
                370             375                 380

agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat aat gat   1203
Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp
            385             390                 395
```

```
aag cta act ttg tgg acc aca cca gac act agt cca aac tgc aca att    1251
Lys Leu Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile
        400             405             410

gct caa gat aag gac tct aaa ctc act ttg gta ctt aca aag tgt gga    1299
Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly
        415             420             425

agt caa ata tta gct aat gtg tct ttg att gtg gtc gca gga aag tac    1347
Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr
430             435             440             445

cac atc ata aat aat aag aca aat cca aaa ata aaa agt ttt act att    1395
His Ile Ile Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile
                450             455             460

aaa ctg cta ttt aat aag aac gga gtg ctt tta gac aac tca aat ctt    1443
Lys Leu Leu Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu
            465             470             475

gga aaa gct tat tgg aac ttt aga agt gga aat tcc aat gtt tcg aca    1491
Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr
            480             485             490

gct tat gaa aaa gca att ggt ttt atg cct aat ttg gta gcg tat cca    1539
Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro
        495             500             505

aaa ccc agt aat tct aaa aaa tat gca aga gac ata gtt tat gga act    1587
Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr
510             515             520             525

ata tat ctt ggt gga aaa cct gat cag cca gca gtc att aaa act acc    1635
Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr
                530             535             540

ttt aac caa gaa act gga tgt gaa tac tct atc aca ttt aac ttt agt    1683
Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser
            545             550             555

tgg tcc aaa acc tat gaa aat gtt gaa ttt gaa acc acc tct ttt acc    1731
Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe Glu Thr Thr Ser Phe Thr
            560             565             570

ttc tcc tat att gcc caa gaa tga aaaagcggcc gctcgagtct agagggcccg    1785
Phe Ser Tyr Ile Ala Gln Glu  *
        575             580


tttaaacccg ctgatcagcc tcgactgtgc cttctagttg ccagccatct gttgtttgcc    1845
cctcccccgt gccttccttg ancctggaan gtgccactcc cactgtcctt tcctaataaa    1905
atgaggaaat gcatc                                                       1920

<210> 53
<211> 580
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Ad5s/Ad37k

<400> 53
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1   5   10   15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20   25   30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
            35   40   45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50   55   60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65   70   75   80
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85   90   95
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
            100   105   110
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
            115   120   125
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130   135   140
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145   150   155   160
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
            165   170   175
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180   185   190
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
            195   200   205
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
    210   215   220
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
            245   250   255
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
            260   265   270
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
            275   280   285
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290   295   300
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
            325   330   335
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
            340   345   350
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
     355   360   365
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370   375   380
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385   390   395   400
Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile Ala Gln Asp
            405   410   415

```
Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
            420             425             430
Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr His Ile Ile
            435             440             445
Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile Lys Leu Leu
        450             455             460
Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu Gly Lys Ala
465             470             475             480
Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr Ala Tyr Glu
            485             490             495
Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro Lys Pro Ser
            500             505             510
Asn Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr Ile Tyr Leu
            515             520             525
Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr Phe Asn Gln
        530             535             540
Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser Trp Ser Lys
545             550             555             560
Thr Tyr Glu Asn Val Glu Phe Glu Thr Thr Ser Phe Thr Phe Ser Tyr
            565             570             575
Ile Ala Gln Glu
            580


<210> 54
<211> 1767
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad5s/Ad37s fiber

<221> CDS
<222> (13)...(1749)

<400> 54
atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc   51
              Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
               1               5                           10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt     99
Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
     15                 20                 25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg    147
Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
30                 35                 40                     45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg    195
Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
                50                 55                 60

ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc agc    243
Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Ser
                65                 70                 75

cta act gta aac cct aag gct cca ctg caa gtt aat act gat tca aac    291
```

```
Leu Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Ser Asn
         80                  85                  90

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta    339
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
         95                 100                 105

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc    387
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
110                 115                 120                 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att    435
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
                130                 135                 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa    483
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
                145                 150                 155

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act    531
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                160                 165                 170

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg    579
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
        175                 180                 185

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg    627
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
190                 195                 200                 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act    675
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
                210                 215                 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act    723
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
                225                 230                 235

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca    771
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
        240                 245                 250

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt    819
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
        255                 260                 265

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag    867
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
270                 275                 280                 285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac    915
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
                290                 295                 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag    963
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
```

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata   1011
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
      320   325   330

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca   1059
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
      335   340   345

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat   1107
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
350   355   360   365

tca aac att ggt ata aat gta aga gca aga gaa ggg ttg aca ttt gac   1155
Ser Asn Ile Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp
              370   375   380

aat gat ggt gcc att aca gta gga aac aaa aat aat gat aag cta act   1203
Asn Asp Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
              385   390   395

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag   1251
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
      400   405   410

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata   1299
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
      415   420   425

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata   1347
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
430   435   440   445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat   1395
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
              450   455   460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt   1443
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
              465   470   475

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga   1491
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
              480   485   490

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc   1539
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
      495   500   505

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa   1587
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
510   515   520   525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac   1635
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
              530   535   540

```
aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc      1683
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
            545                 550                 555

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca      1731
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
            560                 565                 570

tac att gcc caa gaa taa agaagcggcc gcgttatg                          1767
Tyr Ile Ala Gln Glu  *
    575
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<210> 55
<211> 578
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5s/Ad37s

<400> 55
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Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
  1               5                  10                  15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
            35                  40                  45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Ser Leu Thr Val
65                  70                  75                  80
Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Ser Asn Ile Asn Leu
                85                  90                  95
Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu Thr Val Ala
            100                 105                 110
Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr Met Gln Ser
            115                 120                 125
Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile Ala Thr Gln
    130                 135                 140
Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln Thr Ser Gly
145                 150                 155                 160
Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr Ala Ser Pro
                165                 170                 175
Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu Lys Glu Pro
            180                 185                 190
Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly Ala Pro Leu
            195                 200                 205
His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr Gly Pro Gly
    210                 215                 220
Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr Gly Ala Leu
225                 230                 235                 240
Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala Gly Gly Leu
                245                 250                 255
Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val Ser Tyr Pro
            260                 265                 270
```

```
Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln Gly Pro Leu
        275                 280                 285
Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn Lys Gly Leu
        290                 295                 300
Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu Val Asn Leu
305                 310                 315                     320
Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile Ala Ile Asn
                325                 330                 335
Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro Asn Thr Asn
                340                 345                 350
Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp Ser Asn Ile
        355                 360                 365
Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly
        370                 375                 380
Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr Leu Trp Thr
385                 390                 395                     400
Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala
                405                 410                 415
Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr
                420                 425                 430
Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr
        435                 440                 445
Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu
        450                 455                 460
Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly
465                 470                 475                     480
Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro
                485                 490                 495
Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn
                500                 505                 510
Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr
                515                 520                 525
Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro
        530                 535                 540
Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr
545                 550                 555                     560
Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala
                565                 570                 575
Gln Glu
```

<210> 56
<211> 1132
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad37s/Ad5k fiber

<221> CDS
<222> (16)...(1116)

<221> misc_feature
<222> 1125
<223> n = A,T,C or G

<400> 56
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gtcgcaagat ccaag atg aag agg gcc cgg ccc agc gaa gat gac ttc aac    51
                Met Lys Arg Ala Arg Pro Ser Glu Asp Asp Phe Asn
                1           5                   10

ccc gtc tac ccc tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc     99
Pro Val Tyr Pro Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu
            15                  20                  25

act ccc ccc ttt gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg    147
Thr Pro Pro Phe Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly
        30                  35                  40

gta ctg tca ctc aaa ctg gct gat cca atc acc att acc aat ggg gat    195
Val Leu Ser Leu Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp
45                  50                  55                  60

gta tcc ctc aag gtg gga ggt ggt ctc act ttg caa gat gga agc cta    243
Val Ser Leu Lys Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu
                65                  70                  75

act gta aac cct aag gct cca ctg caa gtt aat act gat aaa aaa ctt    291
Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu
                80                  85                  90

gag ctt gca tat gat aat cca ttt gaa agt agt gct aat aaa ctt agt    339
Glu Leu Ala Tyr Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser
            95                  100                 105

tta aaa gta gga cat gga tta aaa gta tta gat gaa aaa agt gct gcg    387
Leu Lys Val Gly His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala
110                 115                 120

ggg tta aaa gat tta att ggc aaa ctt gtg gtt tta aca gga aaa gga    435
Gly Leu Lys Asp Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly
125                 130                 135                 140

ata ggc act gaa aat tta gaa aat aca gat ggt agc agc aga gga att    483
Ile Gly Thr Glu Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile
                145                 150                 155

ggt ata aat gta aga gca aga gaa ggg ttg aca ttt gac aat gat gga    531
Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly
                160                 165                 170

tac ttg gta gca tgg aac cca aag tat gac acg cgc act ttg tgg acc    579
Tyr Leu Val Ala Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr
            175                 180                 185

aca cca gct cca tct cct aac tgt aga cta aat gca gag aaa gat gct    627
Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala
        190                 195                 200

aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata ctt gct aca    675
Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr
205                 210                 215                 220
```

```
gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata tct gga aca    723
Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr
                225             230             235

gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg cta    771
Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu
                240             245             250

cta aac aat tcc ttc ctg gat cca gaa tat tgg aac ttt aga aat gga    819
Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly
                255             260             265

gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg cct    867
Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly·Phe Met Pro
        270             275             280

aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt aac    915
Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn
285             290             295             300

att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta aca    963
Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr
                305             310             ·315

cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act cca    1011
Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro
            320             325             330

agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac tac    1059
Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr
        335             340             345

att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att gcc    1107
Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala
        350             355             360

caa gaa taa agaagcggnc gctcga                                      1132
Gln Glu  *
365
```

<210> 57
<211> 366
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad37s/Ad5k

<400> 57
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Met Lys Arg Ala Arg Pro Ser Glu Asp Asp Phe Asn Pro Val Tyr Pro
1               5               10              15
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
            20              25              30
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
        35              40              45
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
```

```
       50                    55                    60
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
65                    70                    75                    80
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr
                 85                    90                    95
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
              100                   105                   110
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
             115                   120                   125
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
             130                   135                   140
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145                   150                   155                   160
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
                 165                   170                   175
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Ala Pro
              180                   185                   190
Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala Lys Leu Thr Leu
             195                   200                   205
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu
             210                   215                   220
Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr Val Gln Ser Ala
225                   230                   235                   240
His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu Leu Asn Asn Ser
                 245                   250                   255
Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly Asp Leu Thr Glu
              260                   265                   270
Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ser Ala
              275                   280                   285
Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn Ile Val Ser Gln
   290                   295                   300
Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr Leu Thr Ile Thr
305                   310                   315                   320
Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro Ser Ala Tyr Ser
                 325                   330                   335
Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr Ile Asn Glu Ile
              340                   345                   350
Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu
             355                   360                   365


<210> 58
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad37 third repeat

<400> 58
Gly Ser Leu Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp
  1               5                  10                  15


<210> 59
<211> 14
<212> PRT
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<213> Artificial Sequence

<220>
<223> Ad8 last repeat

<400> 59
Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Asp Asn
 1   5   10

<210> 60
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad9 last repeat

<400> 60
Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Asn Asp
 1   5   10

<210> 61
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad15 last repeat

<400> 61
Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Glu Ala
 1   5   10

<210> 62
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Penton region

<400> 62
His Ala Ile Arg Gly Asp Thr Phe
 1   5

<210> 63
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Penton amino acid replacement

<400> 63
Ser Arg Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Ser
1   5   10   15

<210> 64
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Fiber protein conserved sequence

<400> 64
Thr Trp Leu Thr
 1

<210> 65
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> HSP binding motif

<400> 65
Lys Lys Thr Lys
 1

<210> 66
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad8 third repeat

<400> 66
Gly Lys Leu Thr Val Asn Thr Glu Pro Pro Leu His Leu Thr Asn Asn
1   5   10   15

<210> 67
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad9 third repeat

<400> 67
Gly Lys Leu Thr Val Asn Ala Asp Pro Pro Leu Gln Leu Thr Asn Asn
1   5   10   15

<210> 68
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad15 third repeat

<400> 68
Gly Asn Leu Thr Val Asn Thr Glu Pro Pro Leu Gln Leu Thr Asn Asn
 1   5   10   15

<210> 69
<211> 3929
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector pCR2.1

<400> 69
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acgacaggtt tcccgactgg aaagcgggca gtgagcgcaa cgcaattaat gtgagttagc 120
tcactcatta ggcaccccag gctttacact ttatgcttcc ggctcgtatg ttgtgtggaa 180
ttgtgagcgg ataacaattt cacacaggaa acagctatga ccatgattac gccaagcttg 240
gtaccgagct cggatccact agtaacggcc gccagtgtgc tggaattcgg cttaagccga 300
attctgcaga tatccatcac actggcggcc gctcgagcat gcatctagag gcccaattc 360
gccctatagt gagtcgtatt acaattcact ggccgtcgtt ttacaacgtc gtgactggga 420
aaaccctggc gttacccaac ttaatcgcct tgcagcacat ccccctttcg ccagctggcg 480
taatagcgaa gaggcccgca ccgatcgccc ttcccaacag ttgcgcagcc tgaatggcga 540
atggacgcgc cctgtagcgg cgcattaagc gcggcgggtg tggtggttac gcgcagcgtg 600
accgctacac ttgccagcgc cctagcgccc gctcctttcg ctttcttccc ttcctttctc 660
gccacgttcg ccggctttcc ccgtcaagct ctaaatcggg ggctcccttt agggttccga 720
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gggccatcgc cctgatagac ggtttttcgc cctttgacgt tggagtccac gttctttaat 840
agtggactct tgttccaaac tggaacaaca ctcaacccta tctcggtcta ttcttttgat 900
ttataaggga ttttgccgat ttcggcctat tggttaaaaa atgagctgat ttaacaaaaa 960
tttaacgcga attttaacaa aattcagggc gcaagggctg ctaaaggaag cggaacacgt 1020
agaaagccag tccgcagaaa cggtgctgac cccggatgaa tgtcagctac tgggctatct 1080
ggacaaggga aaacgcaagc gcaaagagaa agcaggtagc ttgcagtggg cttacatggc 1140
gatagctaga ctgggcggtt ttatggacag caagcgaacc ggaattgcca gctggggcgc 1200
cctctggtaa ggttgggaag ccctgcaaag taaactggat ggctttcttg ccgccaagga 1260
tctgatggcg caggggatca agatctgatc aagagacagg atgaggatcg tttcgcatga 1320
ttgaacaaga tggattgcac gcaggttctc cggccgcttg ggtggagagg ctattcggct 1380
atgactgggc acaacagaca atcggctgct ctgatgccgc cgtgttccgg ctgtcagcgc 1440
aggggcgccc ggttcttttt gtcaagaccg acctgtccgg tgccctgaat gaactgcagg 1500
acgaggcagc gcggctatcg tggctggcca cgacgggcgt tccttgcgca gctgtgctcg 1560
acgttgtcac tgaagcggga agggactggc tgctattggg cgaagtgccg gggcaggatc 1620
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